GenCore version 4.5

OM protein - protein search, using sw model

Run on: March 1, 2001, 15:46:59 ; Search time 210.42 Seconds
(without alignments)
11.213 Million cell updates/sec

Title: US-09-331-631A-1_COPY_117_185
Perfect score: 384
Sequence: 1 NRQRDPQQQYEQCQKHCQRR.....EEQQREDEEKYEERMKEEDN 69

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_36:*
1: /SIDS1/gcgdata/geneseq/geneseqp/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp/AA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqp/AA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqp/AA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqp/AA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqp/AA1986.DAT:*
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9: /SIDS1/gcgdata/geneseq/geneseqp/AA1988.DAT:*
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11: /SIDS1/gcgdata/geneseq/geneseqp/AA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqp/AA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqp/AA1992.DAT:*
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16: /SIDS1/gcgdata/geneseq/geneseqp/AA1995.DAT:*
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20: /SIDS1/gcgdata/geneseq/geneseqp/AA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqp/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	384	100.0	666	19	W62828	Macadamia integrif
2	367	95.6	666	19	W62829	Macadamia integrif
3	363	94.5	625	19	W62830	Macadamia integrif
4	172	44.8	525	19	W62831	Theobroma cacao an
5	172	44.8	566	13	R20181	Sequence encoded b
6	152	39.6	590	19	W62832	Gossypium hirsutum
7	107	27.9	1162	21	Y58500	HHV8 ORF 73 protei
8	103.5	27.0	1898	20	Y30795	A human trichohyal
9	102.5	26.7	409	20	W90342	G. max truncated S
10	102.5	26.7	489	20	W90341	G. max SBP2 protei
11	101.5	26.4	611	20	Y29039	T. gondii immunoge
12	101	26.3	1135	21	Y68784	Amino acid sequenc
13	101	26.3	1233	20	Y55954	Mouse STE20-relate
14	101	26.3	1239	20	Y55931	Human ZC1 protein.
15	98.5	25.7	1297	20	Y55932	Human ZC2 protein.
16	98.5	25.7	1360	21	Y85263	Human protein kina
17	96	25.0	2023	21	Y54320	Amino acid sequenc
18	95	24.7	444	20	W90340	G. max truncated S
19	95	24.7	482	20	Y07067	Renal cancer assoc
20	95	24.7	524	20	W90339	G. max SBP1 protei
21	94	24.5	562	16	R70491	Leucocytozoan prot
22	93	24.2	200	18	W55301	H. pylori ORF 04ge
23	93	24.2	200	18	W20685	H. pylori secreted
24	93	24.2	529	18	W55444	H. pylori ORF 04cp
25	92.5	24.1	1326	20	Y55933	Human ZC3 protein.
26	91	23.7	2074	21	Y54319	Amino acid sequenc
27	90.5	23.6	740	13	R27530	Plasmodium falcipa
28	90.5	23.6	740	16	R68838	Plasmodium falcipa
29	90	23.4	346	20	Y20115	B. burgdorferi ant
30	90	23.4	373	20	Y20114	B. burgdorferi ant
31	89	23.2	593	19	W62835	Zea mays antimicro
32	88.5	23.0	1299	21	Y58633	Protein regulating
33	88	22.9	360	17	W03627	Human follicle sti
34	88	22.9	412	17	W03626	Human thyrotropin
35	87	22.7	303	15	R60054	Dirofilaria immiti
36	86	22.4	910	20	Y22191	Mouse brain CNG-1
37	85	22.1	432	20	W93954	Human regulatory m
38	85	22.1	1178	18	W30763	Mannose-1-phosphat
39	84.5	22.0	288	20	W72759	Recombinant human
40	84.5	22.0	326	20	Y20119	B. burgdorferi ant
41	84.5	22.0	359	20	Y20118	B. burgdorferi ant
42	84	21.9	301	8	P70867	Sequence of acidic
43	84	21.9	1214	21	Y57444	Mouse Esel protein
44	84	21.9	1715	21	Y57449	Mouse EselL protei
45	83.5	21.7	905	18	W31186	Human p160 polypep

ALIGNMENTS

RESULT 1
W62828
ID W62828 standard; Protein; 666 AA.
XX
AC W62828;
XX
DT 27-OCT-1998 (first entry)
XX
DE Macadamia integrifolia antimicrobial protein.
XX
KW antimicrobial protein; infestation; control.
XX
OS Macadamia integrifolia.
XX
FH Key Location/Qualifiers
FT Peptide 1..28
FT /note= "signal peptide"
FT Protein 29..666
FT /note= "mature protein"
XX
PN WO9827805-A1.
XX
PD 02-JUL-1998.
XX
PF 22-DEC-1997; 97WO-AU00874.
XX
PR 20-DEC-1996; 96AU-0004275.
XX
PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
XX
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
XX
DR WPI; 1998-377279/32.
DR N-PSDB; V42310.
XX

```
PT   Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT   useful for controlling microbial infestations of plants or mammals
XX
PS   Claim 1; Page 34-36; 96pp; English.
XX
CC   The sequence is that of an antimicrobial protein which can
CC   be used to control microbial infestations in plants and mammalian
CC   animals.
XX
SQ   Sequence   666 AA;


  Query Match            100.0%;  Score 384;  DB 19;  Length 666;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-30;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 NRQRDPQQQYEQCQKHCQRRETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDEEKY 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    117 nrqrdpqqqyeqcqkhcqrreteprhmqtcqqrcerryekekrkqqkryeeqqredeeky 176

Qy     61 EERMKEEDN 69
          |||||||||
Db    177 eermkeedn 185


RESULT   2
W62829
ID   W62829 standard; Protein; 666 AA.
XX
AC   W62829;
XX
DT   27-OCT-1998  (first entry)
XX
DE   Macadamia integrifolia antimicrobial protein.
XX
KW   antimicrobial protein; infestation; control.
XX
OS   Macadamia integrifolia.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..28
FT                   /note= "signal peptide"
FT   Protein         29..666
FT                   /note= "mature protein"
XX
PN   WO9827805-A1.
XX
PD   02-JUL-1998.
XX
PF   22-DEC-1997;   97WO-AU00874.
XX
PR   20-DEC-1996;   96AU-0004275.
XX
PA   (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
XX
PI   Bower NI,  Goulter KC,  Green JL,  Manners JM,  Marcus JP;
XX
DR   WPI; 1998-377279/32.
DR   N-PSDB; V42311.
XX
PT   Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT   useful for controlling microbial infestations of plants or mammals
XX
PS   Claim 1; Page 39-41; 96pp; English.
XX
CC   The sequence is that of an antimicrobial protein which can
CC   be used to control microbial infestations in plants and mammalian
CC   animals.
XX
SQ   Sequence   666 AA;


  Query Match            95.6%;  Score 367;  DB 19;  Length 666;
  Best Local Similarity  95.7%;  Pred. No. 1.3e-28;
  Matches   66;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 NRQRDPQQQYEQCQKHCQRRETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDEEKY 60
          |||||||||||||||: ||| ||||||||||||||||||||||||||||||||||||||||
Db    117 nrqrdpqqqyeqcqercqrheteprhmqtcqqrcerryekekrkqqkryeeqqredeeky 176

Qy     61 EERMKEEDN 69
          |||||||||
Db    177 eermkeedn 185


RESULT   3
W62830
ID   W62830 standard; Protein; 625 AA.
XX
AC   W62830;
XX
DT   27-OCT-1998  (first entry)
XX
DE   Macadamia integrifolia antimicrobial protein.
XX
KW   antimicrobial protein; infestation; control.
XX
OS   Macadamia integrifolia.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..28
FT                   /note= "signal peptide"
FT   Protein         29..666
FT                   /note= "mature protein"
XX
PN   WO9827805-A1.
XX
PD   02-JUL-1998.
XX
PF   22-DEC-1997;   97WO-AU00874.
XX
PR   20-DEC-1996;   96AU-0004275.
XX
PA   (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
XX
PI   Bower NI,  Goulter KC,  Green JL,  Manners JM,  Marcus JP;
XX
DR   WPI; 1998-377279/32.
DR   N-PSDB; V42316.
XX
PT   Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT   useful for controlling microbial infestations of plants or mammals
XX
PS   Claim 1; Page 43-45; 96pp; English.
XX
CC   The sequence is that of an antimicrobial protein which can
CC   be used to control microbial infestations in plants and mammalian
CC   animals.
XX
SQ   Sequence   625 AA;


  Query Match            94.5%;  Score 363;  DB 19;  Length 625;
  Best Local Similarity  95.7%;  Pred. No. 3.1e-28;
  Matches   66;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 NRQRDPQQQYEQCQKHCQRRETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDEEKY 60
          |||||||||||||||| |||||||||||| ||||||||||||||||||||||||||||||
Db     76 nrqrdpqqqyeqcqkrcqrreteprhmqicqqrcerryekekrkqqkryeeqqredeeky 135

Qy     61 EERMKEEDN 69
          |||||| ||
Db    136 eermkegdn 144


RESULT   4
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```
W62831
ID   W62831 standard; Protein; 525 AA.
XX
AC   W62831;
XX
DT   27-OCT-1998  (first entry)
XX
DE   Theobroma cacao antimicrobial protein.
XX
KW   antimicrobial protein; infestation; control.
XX
OS   Theobroma cacao.
XX
PN   WO9827805-A1.
XX
PD   02-JUL-1998.
XX
PF   22-DEC-1997;   97WO-AU00874.
XX
PR   20-DEC-1996;   96AU-0004275.
XX
PA   (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
XX
PI   Bower NI,  Goulter KC,  Green JL,  Manners JM,  Marcus JP;
XX
DR   WPI; 1998-377279/32.
XX
PT   Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT   useful for controlling microbial infestations of plants or mammals
XX
PS   Claim 1; Page 47-49; 96pp; English.
XX
CC   The sequence is that of an antimicrobial protein which can
CC   be used to control microbial infestations in plants and mammalian
CC   animals.
XX
SQ   Sequence   525 AA;


  Query Match             44.8%;  Score 172;  DB 19;  Length 525;
  Best Local Similarity   31.4%;  Pred. No. 1.3e-09;
  Matches   32;  Conservative   20;  Mismatches   14;  Indels   36;  Gaps    2;

Qy       3 QRDPQQQYEQCQKHCQRRETEPRHMQTCQQRCERRYEKEKRKQQ---------------- 46
           :|||:|||||||: |:   || |  : |:||||| |::::|:|:
Db      35 erdprqqyeqcqrrceseateereqeqceqrcereykeqqrqqeeelqrqyqqcqgrcqe 94

Qy      47 ----------------KRYEEQQREDEEKY----EERMKEED 68
                           ::|:||:| : | |    : | :||:
Db      95 qqqgqreqqqcqrkcweqykeqergehenyhnhkknrseeee 136


RESULT   5
R20181
ID   R20181 standard; Protein; 566 AA.
XX
AC   R20181;
XX
DT   16-APR-1992  (first entry)
XX
DE   Sequence encoded by 67 kD T. cacao protein cDNA.
XX
KW   Cocoa; flavour; vicilin; seed storage protein.
XX
OS   Theobroma cacao.
XX
PN   WO9119801-A.
XX
PD   26-DEC-1991.
XX
PF   07-JUN-1991;   91WO-GB00914.
XX
PR   11-JUN-1990;   90GB-0013016.
XX
PA   (MRSC ) MARS UK LTD.
XX
PI   Spencer ME,  Hodge R,  Deakin EA,  Ashton S;
XX
DR   WPI; 1992-024418/03.
DR   N-PSDB; Q20377.
XX
PT   Recombinant cocoa proteins - are responsible for flavour in cocoa
PT   beans and produced in large quantities using yeast and bacterial
PT   expression vectors
XX
PS   Claim 4; Fig 2; 59pp; English.
XX
CC   The inventors claim a 67 kD and 31 kD T. cacao protein, and
CC   fragments, and encoding DNAs.  The 47 kD and 31 kD proteins are
CC   derived from the 67 kD precursor.  T. cacao protein cDNA was
CC   detected in a cDNA library prepared from immature cocoa beans RNA
CC   using a probe based on the AA sequence of a CNBr peptide common to
CC   the 47 kD and 31 kD polypeptides.  Homology searches revealed close
CC   homologies between the 67 kD polypeptide and the vicilins, which are
CC   seed storage proteins.
XX
SQ   Sequence   566 AA;


  Query Match             44.8%;  Score 172;  DB 13;  Length 566;
  Best Local Similarity   31.4%;  Pred. No. 1.4e-09;
  Matches   32;  Conservative   20;  Mismatches   14;  Indels   36;  Gaps    2;

Qy       3 QRDPQQQYEQCQKHCQRRETEPRHMQTCQQRCERRYEKEKRKQQ---------------- 46
           :|||:|||||||: |:   || |  : |:||||| |::::|:|:
Db      35 erdprqqyeqcqrrceseateereqeqceqrcereykeqqrqqeeelqrqyqqcqgrcqe 94

Qy      47 ----------------KRYEEQQREDEEKY----EERMKEED 68
                           ::|:||:| : | |    : | :||:
Db      95 qqqgqreqqqcqrkcweqykeqergehenyhnhkknrseeee 136


RESULT   6
W62832
ID   W62832 standard; Protein; 590 AA.
XX
AC   W62832;
XX
DT   27-OCT-1998  (first entry)
XX
DE   Gossypium hirsutum antimicrobial protein.
XX
KW   antimicrobial protein; infestation; control.
XX
OS   Gossypium hirsutum.
XX
PN   WO9827805-A1.
XX
PD   02-JUL-1998.
XX
PF   22-DEC-1997;   97WO-AU00874.
XX
PR   20-DEC-1996;   96AU-0004275.
XX
PA   (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
XX
PI   Bower NI,  Goulter KC,  Green JL,  Manners JM,  Marcus JP;
XX
DR   WPI; 1998-377279/32.
XX
PT   Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT   useful for controlling microbial infestations of plants or mammals
XX
PS   Claim 1; Page 49-51; 96pp; English.
XX
CC   The sequence is that of an antimicrobial protein which can
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CC   be used to control microbial infestations in plants and mammalian
CC   animals.
XX
SQ   Sequence   590 AA;


  Query Match             39.6%;  Score 152;  DB 19;  Length 590;
  Best Local Similarity   34.0%;  Pred. No. 1.4e-07;
  Matches   32;  Conservative   18;  Mismatches   16;  Indels   28;  Gaps    3;

Qy       1 NRQRDPQQQYEQCQKHCQRRETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQ------- 53
           :|  |||::||:||: |  |: | |    ||||| :|:|:|::: |::::| |
Db      78 hrpedpqrryeecqqec--rqqeerqqpqcqqrclkrfeqeqqqsqrqfqecqqhchqqe 135

Qy      54 ----------REDEEKY---------EERMKEED 68
                    ||  |||         ||  :||:
Db     136 qrpekkqqcvrecrekyqenpwrgereeeaeeee 169


RESULT   7
Y58500
ID   Y58500 standard; Protein; 1162 AA.
XX
AC   Y58500;
XX
DT   10-APR-2000  (first entry)
XX
DE   HHV8 ORF 73 protein, SEQ ID NO:21.
XX
KW   HHV8; detection; diagnosis; Kaposi's sarcoma; AIDS; immunogen;
KW   antigen.
XX
OS   Human herpesvirus type 8.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 96
FT                   /label= unknown
XX
PN   WO9961909-A2.
XX
PD   02-DEC-1999.
XX
PF   26-MAY-1999;   99WO-US11407.
XX
PR   26-MAY-1998;   98US-0086695.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Pau CP;
XX
DR   WPI; 2000-097142/08.
XX
PT   New methods and compositions for the detection of human herpesvirus -
XX
PS   Claim 2; Page 59-62; 68pp; English.
XX
CC   Sequences Y58480-Y58532 represent immunogenic polypeptides derived from
CC   human herpes virus type 8 (HHV8, a gammaherpesvirus). HHV8 plays an
CC   important role in the pathogenesis of AIDS-related Kaposi's sarcoma. The
CC   invention relates to a novel method of detecting the presence of human
CC   herpesvirus 8 in a biological sample using peptides representative of
CC   dominant antigenic regions of HHV8. The method comprises contacting one
CC   or more isolated, immunogenic HHV8 peptides with an antibody-containing
CC   biological sample, and detecting the formation of a complex between the
CC   peptide and the antibody. The presence of a peptide-antibody complex
CC   indicates the presence of human herpesvirus 8. The detection of HHV8
CC   infection can be used to diagnose AIDS-associated Kaposi's sarcoma. The
CC   HHV8-specific antibodies are useful therapeutically when for the passive
CC   immunisation of a human against HHV8 infection, thereby reducing HHV8
CC   related disease. The detection assays are highly specific, sensitive and
CC   accurate. Early detection and treatment of Kaposi's sarcoma could
CC   diminish the severity of symptoms related to AIDS and the sensitive
CC   techniques could reduce erroneous characterisations of skin disorders.
CC   Previous assays for HHV8 antibodies such as immunofluorescence assays,
CC   immunoblots and enzyme immunosassays lack the sensitivity and accuracy
CC   needed for reliable diagnosis of Kaposi's sarcoma. Further advantages
CC   of the assays are that reproducible results are obtained and the method
CC   is suitable for rapid throughput and screening of samples economically.
XX
SQ   Sequence   1162 AA;


  Query Match             27.9%;  Score 107;  DB 21;  Length 1162;
  Best Local Similarity   31.3%;  Pred. No. 0.0071;
  Matches   21;  Conservative   25;  Mismatches   21;  Indels    0;  Gaps    0;

Qy       2 RQRDPQQQYEQCQKHCQRRETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDEEKYE 61
           :|:| ||| || |   |: | | :  |  |   |:: |::: :||:: |:||:::::: :
Db     680 qqqdeqqqdeqqqdeqqqdeqeqqdeqeqqdeqeqqdeqqqdeqqqqdeqqqqdeqqqqd 739

Qy      62 ERMKEED 68
           |: ::::
Db     740 eqqqqde 746


RESULT   8
Y30795
ID   Y30795 standard; Protein; 1898 AA.
XX
AC   Y30795;
XX
DT   25-NOV-1999  (first entry)
XX
DE   A human trichohyalin (TRHY) protein.
XX
KW   Human; trichohyalin; TRHY; protein; tissue structure; wound healing;
KW   terminally differentiating epidermal tissue; proteinaceous gel;
KW   breast implant.
XX
OS   Homo sapiens.
XX
PN   US5958752-A.
XX
PD   28-SEP-1999.
XX
PF   14-FEB-1997;   97US-0800644.
XX
PR   30-APR-1993;   93US-0056200.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Kim I,  Chung S,  Park S,  Steinert PM,  Lee S;
XX
DR   WPI; 1999-561041/47.
DR   N-PSDB; Z22301.
XX
PT   Human trichohyalin useful for forming a proteinaceous gel that promotes
PT   wound healing -
XX
PS   Disclosure; Fig 3A-W; 126pp; English.
XX
CC   The present sequence represents a human trichohyalin (TRHY) protein.
CC   The protein is found in terminally differentiating epidermal tissue,
CC   and is involved in forming the structural architecture of such
CC   tissue. The trichohyalin protein is useful for forming a
CC   proteinaceous gel which may then be used for healing wounds, or in
CC   breast implants.
XX
SQ   Sequence   1898 AA;


  Query Match             27.0%;  Score 103.5;  DB 20;  Length 1898;
  Best Local Similarity   36.2%;  Pred. No. 0.026;
  Matches   25;  Conservative   19;  Mismatches   18;  Indels    7;  Gaps    3;

Qy       2 RQRDPQQQYE-QCQKHCQRRETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQ--REDEE 58
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          || : |||   : ::  :|:: | |     :|: ||| ::|:|:||:   |||  || ||
Db    290 rqeeeqqqqrlrreqqlrrkqeeerr----eqqeerreqqerreqqeerreqqlrreqee 345

Qy     59 KYEERMKEE 67
          : |:::: |
Db    346 rreqqlrre 354
```

RESULT 9
W90342
ID W90342 standard; protein; 409 AA.
XX
AC W90342;
XX
DT 24-MAY-1999 (first entry)
XX
DE G. max truncated SBP2 protein.
XX
KW SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;
KW seed; carbohydrate content; soybean.
XX
OS Glycine max.
XX
PN WO9853086-A1.
XX
PD 26-NOV-1998.
XX
PF 21-MAY-1998; 98WO-US10465.
XX
PR 22-MAY-1997; 97US-0047568.
XX
PA (UNIW) UNIV WASHINGTON STATE RES FOUND.
XX
PI Chao WS, Grimes HD;
XX
DR WPI; 1999-070155/06.
XX
PT New modified plant sucrose binding proteins - used to develop
PT transgenic plants which can have enhanced or decreased sucrose
PT uptake activity in developing seeds
XX
PS Claim 7; Page 39-40; 58pp; English.
XX
CC This sequence represents a novel sucrose binding protein, SBP2 isolated
CC from Glycine max. This protein is used in a method resulting in the
CC production of a modified plant sucrose binding protein (SBP) which has a
CC modified amino acid sequence compared to a corresponding wild-type SBP,
CC and where expression of the modified SBP in a yeast assay system confers
CC enhanced sucrose uptake compared to the corresponding wild-type SBP.
CC The products of the invention can be used for producing transgenic plants
CC which have modified sucrose uptake activity, particularly in developing
CC seeds. Enhanced sucrose uptake activity in developing seeds may be
CC desirable where it is an advantage to increase the carbohydrate content
CC of the seed (e.g. where the seed is the primary plant material harvested,
CC such as soybean). In contrast, decreased sucrose uptake activity in
CC seeds might be desirable where the vegetative material of the plant is
CC harvested. The SBP regulatory regions confer specific or enhanced
CC expression in developing seeds and so may be used to express any
CC transgene in developing seeds.
XX
SQ Sequence 409 AA;

```
  Query Match             26.7%;  Score 102.5;  DB 20;  Length 409;
  Best Local Similarity   36.2%;  Pred. No. 0.0067;
  Matches   21;  Conservative   18;  Mismatches   12;  Indels    7;  Gaps    2;

Qy     12 QCQKHCQRRETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDEEKYEERMKEEDN 69
          |||:  |  |:: |   || |:|    :  |::::|: ||: || ||:::|: :|||::
Db     45 qcqqqrqytesdkr---tclqqc----dsmkqerekqveeetrekeeehqeqheeeed 95
```

RESULT 10
W90341
ID W90341 standard; protein; 489 AA.
XX
AC W90341;
XX
DT 24-MAY-1999 (first entry)
XX
DE G. max SBP2 protein.
XX
KW SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;
KW seed; carbohydrate content; soybean.
XX
OS Glycine max.
XX
PN WO9853086-A1.
XX
PD 26-NOV-1998.
XX
PF 21-MAY-1998; 98WO-US10465.
XX
PR 22-MAY-1997; 97US-0047568.
XX
PA (UNIW) UNIV WASHINGTON STATE RES FOUND.
XX
PI Chao WS, Grimes HD;
XX
DR WPI; 1999-070155/06.
XX
PT New modified plant sucrose binding proteins - used to develop
PT transgenic plants which can have enhanced or decreased sucrose
PT uptake activity in developing seeds
XX
PS Claim 13b; Page 37-38; 58pp; English.
XX
CC This sequence represents a novel sucrose binding protein, SBP2 isolated
CC from Glycine max. This protein is used in a method resulting in the
CC production of a modified plant sucrose binding protein (SBP) which has a
CC modified amino acid sequence compared to a corresponding wild-type SBP,
CC and where expression of the modified SBP in a yeast assay system confers
CC enhanced sucrose uptake compared to the corresponding wild-type SBP.
CC The products of the invention can be used for producing transgenic plants
CC which have modified sucrose uptake activity, particularly in developing
CC seeds. Enhanced sucrose uptake activity in developing seeds may be
CC desirable where it is an advantage to increase the carbohydrate content
CC of the seed (e.g. where the seed is the primary plant material harvested,
CC such as soybean). In contrast, decreased sucrose uptake activity in
CC seeds might be desirable where the vegetative material of the plant is
CC harvested. The SBP regulatory regions confer specific or enhanced
CC expression in developing seeds and so may be used to express any
CC transgene in developing seeds.
XX
SQ Sequence 489 AA;

```
  Query Match             26.7%;  Score 102.5;  DB 20;  Length 489;
  Best Local Similarity   36.2%;  Pred. No. 0.008;
  Matches   21;  Conservative   18;  Mismatches   12;  Indels    7;  Gaps    2;

Qy     12 QCQKHCQRRETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDEEKYEERMKEEDN 69
          |||:  |  |:: |   || |:|    :  |::::|: ||: || ||:::|: :|||::
Db     45 qcqqqrqytesdkr---tclqqc----dsmkqerekqveeetrekeeehqeqheeeed 95
```

RESULT 11
Y29039
ID Y29039 standard; Protein; 611 AA.
XX
AC Y29039;
XX
DT 24-SEP-1999 (first entry)
XX
DE T. gondii immunogenic protein.
XX

```
KW   Immunogenic protein; Toxoplasma gondii protein; oocyst shedding; cat;
KW   T. gondii infection; enteric apicomplexa oocyst; Cryptosporidium oocyst;
KW   Toxoplasma oocyst.
XX
OS   Toxoplasma gondii.
XX
PN   WO9932633-A1.
XX
PD   01-JUL-1999.
XX
PF   18-DEC-1998;   98WO-US27137.
XX
PR   19-DEC-1997;   97US-0994825.
XX
PA   (HESK-) HESKA CORP.
XX
PI   Lutz SB,  Milhausen MJ,  Ng RK;
XX
DR   WPI; 1999-418930/35.
DR   N-PSDB; X91242.
XX
PT   New isolated Toxoplasma gondii nucleic acids used, e.g. to treat
PT   infection caused by this microorganism
XX
PS   Claim 29; Page 227-229; 381pp; English.
XX
CC   The invention provides isolated Toxoplasma gondii nucleic acids that
CC   encode immunogenic polypeptides. The T. gondii nucleic acid molecules,
CC   immunogenic proteins and antibodies to the proteins can be used to
CC   inhibit T. gondii oocyst shedding in a cat due to infection with
CC   T. gondii. They can be used for preventing T. gondii infection and for
CC   preventing the spread of T. gondii infection. They can also be used for
CC   detecting T. gondii infection. The detection method can be used to detect
CC   parasite cysts or oocysts in feces, e.g. from enteric apicomplexa oocysts
CC   such as Cryptosporidium oocysts and Toxoplasma oocysts.
XX
SQ   Sequence   611 AA;


  Query Match             26.4%;  Score 101.5;  DB 20;  Length 611;
  Best Local Similarity   33.8%;  Pred. No. 0.013;
  Matches   25;  Conservative   19;  Mismatches   23;  Indels    7;  Gaps    2;

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Db     378 rqreeeeererrrveeekarqreeeeererrrveeekarqreeeeeregrrveeekarqr 437

Qy      55 EDEEKYEERMKEED 68
           |:||: | |  ||:
Db     438 eeeeeregrrveee 451


RESULT  12
Y68784
ID   Y68784 standard; Protein; 1135 AA.
XX
AC   Y68784;
XX
DT   16-MAY-2000  (first entry)
XX
DE   Amino acid sequence of a human phosphorylation effector PHSP-16.
XX
KW   Human; phosphorylation effector; PHSP; proliferative disorder;
KW   immune disorder; neuronal disorder.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   9
FT                   /note= "potential phosphorylation site"
FT   Modified-site   17
FT                   /note= "potential phosphorylation site"
FT   Region          31..54
FT                   /note= "protein kinase signature sequence"
FT   Modified-site   33
FT                   /note= "potential glycosylation site"
FT   Modified-site   59
FT                   /note= "potential phosphorylation site"
FT   Modified-site   59
FT                   /note= "potential phosphorylation site"
FT   Modified-site   77
FT                   /note= "potential phosphorylation site"
FT   Modified-site   112
FT                   /note= "potential phosphorylation site"
FT   Modified-site   124
FT                   /note= "potential phosphorylation site"
FT   Region          129..182
FT                   /note= "protein kinase signature sequence"
FT   Region          149..161
FT                   /note= "protein kinase signature sequence"
FT   Modified-site   187
FT                   /note= "potential phosphorylation site"
FT   Active-site     190..200
FT                   /note= "tyrosine kinase catalytic site"
FT   Active-site     214..236
FT                   /note= "tyrosine kinase catalytic site"
FT   Modified-site   222
FT                   /note= "potential phosphorylation site"
FT   Modified-site   255
FT                   /note= "potential phosphorylation site"
FT   Modified-site   259
FT                   /note= "potential phosphorylation site"
FT   Modified-site   264
FT                   /note= "potential phosphorylation site"
FT   Modified-site   309
FT                   /note= "potential phosphorylation site"
FT   Modified-site   319
FT                   /note= "potential phosphorylation site"
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FT                   /note= "potential phosphorylation site"
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FT                   /note= "potential phosphorylation site"
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FT                   /note= "potential phosphorylation site"
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FT                   /note= "potential phosphorylation site"
FT   Modified-site   550
FT                   /note= "potential phosphorylation site"
FT   Modified-site   554
FT                   /note= "potential phosphorylation site"
FT   Modified-site   570
FT                   /note= "potential glycosylation site"
FT   Modified-site   572
FT                   /note= "potential phosphorylation site"
FT   Modified-site   624
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FT                   /note= "potential phosphorylation site"
FT   Modified-site   632
FT                   /note= "potential phosphorylation site"
FT   Modified-site   681
FT                   /note= "potential phosphorylation site"
FT   Modified-site   682
FT                   /note= "potential phosphorylation site"
FT   Modified-site   688
FT                   /note= "potential phosphorylation site"
FT   Modified-site   689
FT                   /note= "potential phosphorylation site"
FT   Modified-site   706
FT                   /note= "potential phosphorylation site"
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FT   Modified-site   718
FT                   /note= "potential glycosylation site"
FT   Modified-site   720
FT                   /note= "potential phosphorylation site"
FT   Modified-site   726
FT                   /note= "potential phosphorylation site"
FT   Modified-site   811
FT                   /note= "potential phosphorylation site"
FT   Modified-site   815
FT                   /note= "potential phosphorylation site"
FT   Domain          836..1115
FT                   /note= "NIK1-like kinase domain"
FT   Modified-site   898
FT                   /note= "potential phosphorylation site"
FT   Modified-site   931
FT                   /note= "potential phosphorylation site"
FT   Modified-site   958
FT                   /note= "potential phosphorylation site"
FT   Modified-site   978
FT                   /note= "potential phosphorylation site"
FT   Modified-site   999
FT                   /note= "potential phosphorylation site"
FT   Modified-site   1012
FT                   /note= "potential phosphorylation site"
FT   Modified-site   1067
FT                   /note= "potential glycosylation site"
FT   Modified-site   1113
FT                   /note= "potential phosphorylation site"
XX
PN   WO200006728-A2.
XX
PD   10-FEB-2000.
XX
PF   28-JUL-1999;   99WO-US17132.
XX
PR   28-JUL-1998;   98US-0123494.
PR   14-SEP-1998;   98US-0152814.
PR   14-OCT-1998;   98US-0173482.
PR   03-NOV-1998;   98US-0106889.
PR   19-NOV-1998;   98US-0109093.
PR   22-DEC-1998;   98US-0113796.
PR   12-JAN-1999;   99US-0173482.
PR   12-JAN-1999;   99US-0229005.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Hillman JL,  Lal P,  Tang YT,  Corley NC,  Guegler KJ,  Baughn MR;
PI   Patterson C,  Bandman O,  Au-Young J,  Gorgone GA,  Yue H,  Azimzai Y;
PI   Reddy R,  Lu DAM,  Shih LL;
XX
DR   WPI; 2000-183125/16.
DR   N-PSDB; Z46153.
XX
PT   New human phosphorylation effectors useful for the diagnosis, treatment
PT   and prevention of proliferative, immune and neuronal disorders  -
XX
PS   Claim 1; Page 98-100; 142pp; English.
XX
CC   Y68769-95 and Y68797-99 represent human phosphorylation effectors (PHSP),
CC   designated PHSP1-PHSP31 (the protein sequence for PHSP28 is not given
CC   in the specification). The sequences were isolated from cDNA libraries
CC   prepared from various human tissues. The PHSP proteins are useful for
CC   the diagnosis, treatment and prevention of proliferative disorders,
CC   immune disorders and neuronal disorders. The PHSP proteins form
CC   pharmaceutical compositions which useful for treating or preventing
CC   disorders associated with decreased PHSP expression/activity. PHSP
CC   antagonists are useful for treating or preventing disorders associated
CC   with increased PHSP expression/activity.
XX
SQ   Sequence   1135 AA;

 Query Match             26.3%;  Score 101;  DB 21;  Length 1135;
```

```
  Best Local Similarity   36.1%;  Pred. No. 0.027;
  Matches   30;  Conservative   16;  Mismatches   19;  Indels   18;  Gaps    4;

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           ||:  :|| || ::    |||| | |  |  :||  || ::|||:    :::| ||::|
Db     395 rqkrieqqkeqrrrleeqqrrerearrqqereqr--rreqeekrrleelerrrkeeeerr 452

Qy      55 ---------EDEEKYEERMKEED 68
                   | |::|  |  ||:
Db     453 raeeekrrvereqeyirrqleee 475


RESULT  13
Y55954
ID   Y55954 standard; Protein; 1233 AA.
XX
AC   Y55954;
XX
DT   18-FEB-2000  (first entry)
XX
DE   Mouse STE20-related protein kinase NIK_m.
XX
KW   Antirheumatic; antiathritic; antiinflammatory; antiallergic; osteopathic;
KW   antipsoriatic; antiarteriosclerotic; antiasthmatic; immunosupressive;
KW   neuroprotective; cardiant; cerebroprotective; cytostatic; antidiabetic;
KW   vulnery; STE20; protein kinase; STLK2; STLK3; STLK4; STLK5, STLK6, STLK7;
KW   ZC1, ZC2, ZC3, ZC4, KHS2, SULU1, SULU3, GEK2, PAK4; PAK5; antagonist;
KW   antibody; gene therapy; rheumatoid arthritis; artherosclerosis; asthma;
KW   inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;
KW   rhinitis; autoimmunity; organ transplantation; multiple sclerosis;
KW   myocardial infarction; cardiovascular disease; stroke; renal failure;
KW   oxidative stress-related neurodegenerative disorder; Parkinson's disease;
KW   amylotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy;
KW   ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;
KW   mesangial disorder; growth regulation; wound healing; T cell activation;
KW   immunosuppressant.
XX
OS   Mus sp.
XX
PN   WO9953036-A2.
XX
PD   21-OCT-1999.
XX
PF   13-APR-1999;   99WO-US08150.
XX
PR   14-APR-1998;   98US-0081784.
XX
PA   (SUGE-) SUGEN INC.
XX
PI   Plowman G,  Martinez R,  Whyte D;
XX
DR   WPI; 1999-611301/52.
XX
PT   Novel kinase-related polypeptides used for the diagnosis and treatment
PT   of kinase-related diseases and disorders  -
XX
PS   Disclosure; Page 339-343; 387pp; English.
XX
CC   This sequence represents a novel STE20-related protein kinase. The
CC   invention relates to nucleic acid molecule encoding a kinase polypeptide
CC   selected from STLK2, STLK3, STLK4, STLK5, STLK6, STLK7, ZC1, ZC2, ZC3,
CC   ZC4, KHS2, SULU1, SULU3, GEK2, PAK4 and PAK5. The proteins are used to
CC   identify agonists and antagonists, and to raise antibodies. The
CC   polynucleotides are useful in gene therapy protocols.The polynucleotides,
CC   polypeptides, antibodies, antagonists and agonists may be used to treat
CC   diseases such as immune-related disorders and diseases (e.g. rheumatoid
CC   arthritis, artherosclerosis, chronic inflammatory bowel disease (e.g.
CC   Crohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis,
CC   rhinitis, autoimmunity, and organ transplantation, chronic inflammatory
CC   pelvic disease, multiple sclerosis, organ transplantation, myocardial
CC   infarction, cardiovascular disease, stroke, renal failure, oxidative
CC   stress-related neurodegenerative disorders (e.g. amylotrophic lateral
CC   sclerosis, Parkinson's disease and Leigh syndrome), cancer,
```

```
CC   cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes
CC   mellitus, fibrotic and mesangial disorders. The proteins may also be
CC   useful for cell growth regulation (e.g. in wound healing), T cell
CC   activation, mitosis control, and as immunosuppressants.
XX
SQ   Sequence   1233 AA;


  Query Match             26.3%;  Score 101;  DB 20;  Length 1233;
  Best Local Similarity   36.1%;  Pred. No. 0.029;
  Matches   30;  Conservative   16;  Mismatches   19;  Indels   18;  Gaps    4;

Qy       2 RQRDPQQQYEQCQK--HCQRRETEPRHMQTCQQRCERRYEKEKRK----QQKRYEEQQR- 54
           ||:  :|| || ::    |||| | |  |  :||  || ::|||:    :::| ||::|
Db     394 rqkrieqqkeqrrrleeqqrrerearrqqereqr--rreqeekrrleelerrrkeeeerr 451

Qy      55 ---------EDEEKYEERMKEED 68
                   | |::|  |  ||:
Db     452 raeeekrrvereqeyirrqleee 474


RESULT  14
Y55931
ID   Y55931 standard; Protein; 1239 AA.
XX
AC   Y55931;
XX
DT   18-FEB-2000  (first entry)
XX
DE   Human ZC1 protein.
XX
KW   Antirheumatic; antiathritic; antiinflammatory; antiallergic; osteopathic;
KW   antipsoriatic; antiarteriosclerotic; antiasthmatic; immunosupressive;
KW   neuroprotective; cardiant; cerebroprotective; cytostatic; antidiabetic;
KW   vulnery; STE20; protein kinase; STLK2; STLK3; STLK4; STLK5, STLK6, STLK7;
KW   ZC1, ZC2, ZC3, ZC4, KHS2, SULU1, SULU3, GEK2, PAK4; PAK5; antagonist;
KW   antibody; gene therapy; rheumatoid arthritis; artherosclerosis; asthma;
KW   inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;
KW   rhinitis; autoimmunity; organ transplantation; multiple sclerosis;
KW   myocardial infarction; cardiovascular disease; stroke; renal failure;
KW   oxidative stress-related neurodegenerative disorder; Parkinson's disease;
KW   amylotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy;
KW   ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;
KW   mesangial disorder; growth regulation; wound healing; T cell activation;
KW   immunosuppressant.
XX
OS   Homo sapiens.
XX
PN   WO9953036-A2.
XX
PD   21-OCT-1999.
XX
PF   13-APR-1999;   99WO-US08150.
XX
PR   14-APR-1998;   98US-0081784.
XX
PA   (SUGE-) SUGEN INC.
XX
PI   Plowman G,  Martinez R,  Whyte D;
XX
DR   WPI; 1999-611301/52.
DR   N-PSDB; Z40483.
XX
PT   Novel kinase-related polypeptides used for the diagnosis and treatment
PT   of kinase-related diseases and disorders  -
XX
PS   Claim 11; Page 269-274; 387pp; English.
XX
CC   This sequence represents a novel STE20-related protein kinase. The
CC   invention relates to nucleic acid molecule encoding a kinase polypeptide
CC   selected from STLK2, STLK3, STLK4, STLK5, STLK6, STLK7, ZC1, ZC2, ZC3,
CC   ZC4, KHS2, SULU1, SULU3, GEK2, PAK4 and PAK5. The proteins are used to
CC   identify agonists and antagonists, and to raise antibodies. The
CC   polynucleotides are useful in gene therapy protocols.The polynucleotides,
CC   polypeptides, antibodies, antagonists and agonists may be used to treat
CC   diseases such as immune-related disorders and diseases (e.g. rheumatoid
CC   arthritis, artherosclerosis, chronic inflammatory bowel disease (e.g.
CC   Crohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis,
CC   rhinitis, autoimmunity, and organ transplantation, chronic inflammatory
CC   pelvic disease, multiple sclerosis, organ transplantation, myocardial
CC   infarction, cardiovascular disease, stroke, renal failure, oxidative
CC   stress-related neurodegenerative disorders (e.g. amylotrophic lateral
CC   sclerosis, Parkinson's disease and Leigh syndrome), cancer,
CC   cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes
CC   mellitus, fibrotic and mesangial disorders. The proteins may also be
CC   useful for cell growth regulation (e.g. in wound healing), T cell
CC   activation, mitosis control, and as immunosuppressants.
XX
SQ   Sequence   1239 AA;


  Query Match             26.3%;  Score 101;  DB 20;  Length 1239;
  Best Local Similarity   36.1%;  Pred. No. 0.03;
  Matches   30;  Conservative   16;  Mismatches   19;  Indels   18;  Gaps    4;

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           ||:  :|| || ::    |||| | |  |  :||  || ::|||:    :::| ||::|
Db     395 rqkrieqqkeqrrrleeqqrrerearrqqereqr--rreqeekrrleelerrrkeeeerr 452

Qy      55 ---------EDEEKYEERMKEED 68
                   | |::|  |  ||:
Db     453 raeeekrrvereqeyirrqleee 475


RESULT  15
Y55932
ID   Y55932 standard; Protein; 1297 AA.
XX
AC   Y55932;
XX
DT   18-FEB-2000  (first entry)
XX
DE   Human ZC2 protein.
XX
KW   Antirheumatic; antiathritic; antiinflammatory; antiallergic; osteopathic;
KW   antipsoriatic; antiarteriosclerotic; antiasthmatic; immunosupressive;
KW   neuroprotective; cardiant; cerebroprotective; cytostatic; antidiabetic;
KW   vulnery; STE20; protein kinase; STLK2; STLK3; STLK4; STLK5, STLK6, STLK7;
KW   ZC1, ZC2, ZC3, ZC4, KHS2, SULU1, SULU3, GEK2, PAK4; PAK5; antagonist;
KW   antibody; gene therapy; rheumatoid arthritis; artherosclerosis; asthma;
KW   inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;
KW   rhinitis; autoimmunity; organ transplantation; multiple sclerosis;
KW   myocardial infarction; cardiovascular disease; stroke; renal failure;
KW   oxidative stress-related neurodegenerative disorder; Parkinson's disease;
KW   amylotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy;
KW   ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;
KW   mesangial disorder; growth regulation; wound healing; T cell activation;
KW   immunosuppressant.
XX
OS   Homo sapiens.
XX
PN   WO9953036-A2.
XX
PD   21-OCT-1999.
XX
PF   13-APR-1999;   99WO-US08150.
XX
PR   14-APR-1998;   98US-0081784.
XX
PA   (SUGE-) SUGEN INC.
XX
PI   Plowman G,  Martinez R,  Whyte D;
XX
DR   WPI; 1999-611301/52.
DR   N-PSDB; Z40484.
XX
```

PT Novel kinase-related polypeptides used for the diagnosis and treatment
PT of kinase-related diseases and disorders -
XX
PS Claim 11; Page 274-278; 387pp; English.
XX
CC This sequence represents a novel STE20-related protein kinase. The
CC invention relates to nucleic acid molecule encoding a kinase polypeptide
CC selected from STLK2, STLK3, STLK4, STLK5, STLK6, STLK7, ZC1, ZC2, ZC3,
CC ZC4, KHS2, SULU1, SULU3, GEK2, PAK4 and PAK5. The proteins are used to
CC identify agonists and antagonists, and to raise antibodies. The
CC polynucleotides are useful in gene therapy protocols.The polynucleotides,
CC polypeptides, antibodies, antagonists and agonists may be used to treat
CC diseases such as immune-related disorders and diseases (e.g. rheumatoid
CC arthritis, artherosclerosis, chronic inflammatory bowel disease (e.g.
CC Crohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis,
CC rhinitis, autoimmunity, and organ transplantation, chronic inflammatory
CC pelvic disease, multiple sclerosis, organ transplantation, myocardial
CC infarction, cardiovascular disease, stroke, renal failure, oxidative
CC stress-related neurodegenerative disorders (e.g. amylotrophic lateral
CC sclerosis, Parkinson's disease and Leigh syndrome), cancer,
CC cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes
CC mellitus, fibrotic and mesangial disorders. The proteins may also be
CC useful for cell growth regulation (e.g. in wound healing), T cell
CC activation, mitosis control, and as immunosuppressants.
XX
SQ Sequence 1297 AA;

Query Match 25.7%; Score 98.5; DB 20; Length 1297;
Best Local Similarity 34.1%; Pred. No. 0.054;
Matches 28; Conservative 17; Mismatches 16; Indels 21; Gaps 5;

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Qy      58 E-----------KYEERMKEED 68
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Db     380 elrkqqereqrrhyeeqmrree 401
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Search completed: March 1, 2001, 15:47:01
Job time: 226 sec